S. Prasad

**CRF Err᠁ Corrected by the STIC Syst᠁ms ᠁anch**

Serial Numb᠁r: ___09/714,792___

CRF Processing Dat : 4/10/2002
Edited by: _____
Verified by: _____ (STIC staff)

**ENTERED**

☐ Changed a file from non-ASCII to ASCII.

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☑ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A) Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: __4__

☐ Other: _____

_____

_____

**\*Examin᠁r: The abov᠁ corrections must b᠁ communicated to the applicant in th᠁ first Offic᠁ Action. DO NOT send a copy of this form.**

3/1/95

1646

RAW SEQUENCE LISTING                    DATE: 04/10/2002
PATENT APPLICATION:  US/09/714,792      TIME: 18:20:44

Input Set : **N:\jumbos\714792.txt**
Output Set: **N:\CRF3\04102002\I714792.raw**

**SEQUENCE LISTING**
```
 4 (1) GENERAL INFORMATION:
 6       (i) APPLICANT: Collins, Mary
 7                     Donaldson, Debra
 8                     Fitz, Lori
 9                     Neben, Tamlyn
10                     Whitters, Matthew
11                     Wood, Clive
13      (ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
15     (iii) NUMBER OF SEQUENCES: 9
17      (iv) CORRESPONDENCE ADDRESS:
18           (A) ADDRESSEE: Genetics Institute, Inc.
19           (B) STREET: 87 CambridgePark Drive
20           (C) CITY: Cambridge
21           (D) STATE: MA
22           (E) COUNTRY: USA
23           (F) ZIP: 02140
25       (v) COMPUTER READABLE FORM:
26           (A) MEDIUM TYPE: Floppy disk
27           (B) COMPUTER: IBM PC compatible
28           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
29           (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
31      (vi) CURRENT APPLICATION DATA:
C--> 32           (A) APPLICATION NUMBER: US/09/714,792
C--> 33           (B) FILING DATE: 16-Nov-2000
34           (C) CLASSIFICATION:
36    (viii) ATTORNEY/AGENT INFORMATION:
37           (A) NAME: Brown, Scott A.
38           (B) REGISTRATION NUMBER: 32,724
39           (C) REFERENCE/DOCKET NUMBER: GI5268
41      (ix) TELECOMMUNICATION INFORMATION:
42           (A) TELEPHONE: (617) 498-8224
43           (B) TELEFAX: (617) 876-5851
46 (2) INFORMATION FOR SEQ ID NO: 1:
48       (i) SEQUENCE CHARACTERISTICS:
49           (A) LENGTH: 1525 base pairs
50           (B) TYPE: nucleic acid
51           (C) STRANDEDNESS: double
52           (D) TOPOLOGY: linear
54      (ii) MOLECULE TYPE: cDNA
56     (iii) HYPOTHETICAL: NO
59      (ix) FEATURE:
60           (A) NAME/KEY: CDS
```

```
61          (B) LOCATION: 256..1404
64     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66   GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAG AGAGAGAGAA AGATTGCTTG      60
68   CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA TAAGGAAGGA     120
70   AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG GTCTTGTGAT     180
72   AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA     240
74   CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT      291
75                     Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
76                      1               5                  10
78   CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT      339
79   Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
80           15                  20                  25
82   CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT      387
83   Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
84        30                  35                  40
86   TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA      435
87   Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
88   45                  50                  55                  60
90   CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG      483
91   Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
92                   65                  70                  75
94   ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT      531
95   Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn
96              80                  85                  90
98   AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA      579
99   Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr
100             95                 100                 105
102  AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA      627
103  Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile
104      110                 115                 120
106  TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA      675
107  Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile
108  125                 130                 135                 140
110  TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA      723
111  Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr
112                  145                 150                 155
114  GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG      771
115  Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu
116                  160                 165                 170
118  GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT      819
119  Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn
120             175                 180                 185
122  GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT      867
123  Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe
124      190                 195                 200
126  TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC      915
127  Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser
128  205                 210                 215                 220
130  TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA      963
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131    Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu
132                    225                 230                 235
134    TTC CTT CAT ATT AGT GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG      1011
135    Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp
136                    240                 245                 250
138    AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT      1059
139    Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile
140                    255                 260                 265
142    GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC      1107
143    Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn
144            270                 275                 280
146    GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT      1155
147    Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe
148    285                 290                 295                 300
150    TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG      1203
151    Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp
152                    305                 310                 315
154    AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC      1251
155    Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp
156                    320                 325                 330
158    TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT      1299
159    Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu
160            335                 340                 345
162    TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA      1347
163    Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
164            350                 355                 360
166    TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT      1395
167    Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
168    365                 370                 375                 380
170    ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG             1444
171    Thr Leu Cys
174    TCATATTAAA CTCAATTTCT CTTAAAATTT CGAATACATC TTCTTGAAAA TCCAAAAAAA    1504
176    AAAAAAAAAA AAAAACTCGA G                                            1525
179    (2) INFORMATION FOR SEQ ID NO: 2:
181         (i) SEQUENCE CHARACTERISTICS:
182              (A) LENGTH: 383 amino acids
183              (B) TYPE: amino acid
184              (D) TOPOLOGY: linear
186         (ii) MOLECULE TYPE: protein
188         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
190    Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile Leu Leu Cys Thr
191    1               5                   10                  15
193    Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
194                    20                  25                  30
196    Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys
197            35                  40                  45
199    Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu
200    50                  55                  60
202    Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr
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Input Set : N:\jumbos\714792.txt
Output Set: N:\CRF3\04102002\I714792.raw

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203    65                      70                      75                      80
205    Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
206                    85                      90                      95
208    Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu
209                    100                     105                     110
211    Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly
212                    115                     120                     125
214    Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp
215        130                     135                     140
217    Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp
218    145                     150                     155                     160
220    Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu
221                    165                     170                     175
223    Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys
224                    180                     185                     190
226    Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val
227                    195                     200                     205
229    Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe
230        210                     215                     220
232    Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile
233    225                     230                     235                     240
235    Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly
236·                   245                     250                     255
238    Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu
239                    260                     265                     270
241    Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu
242        275                     280                     285
244    Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys
245        290                     295                     300
247    Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser
248    305                     310                     315                     320
250    Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile
251                    325                     330                     335
253    Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu
254        340                     345                     350
256    Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His
257        355                     360                     365
259    Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys
260        370                     375                     380
262 (2) INFORMATION FOR SEQ ID NO: 3:
264      (i) SEQUENCE CHARACTERISTICS:
265          (A) LENGTH: 1369 base pairs
266          (B) TYPE: nucleic acid
267          (C) STRANDEDNESS: double
268          (D) TOPOLOGY: linear
270      (ii) MOLECULE TYPE: cDNA
272      (iii) HYPOTHETICAL: NO
275      (ix) FEATURE:
276          (A) NAME/KEY: CDS
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277        (B) LOCATION: 103..1245
280     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
282  GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC      60
284  GGCGGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC GTT        114
285                                                 Met Ala Phe Val
286       /                                          1
288  TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT      162
289  Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
290   5                 10                  15                  20
292  GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG      210
293  Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
294                     25                  30                  35
296  GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA      258
297  Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
298                 40                  45                  50
300  TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA      306
301  Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
302             55                  60                  65
304  TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC      354
305  Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
306         70                  75                  80
308  ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC      402
309  Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
310   85                  90                  95                 100
312  ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA      450
313  Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
314                     105                 110                 115
316  TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA      498
317  Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro
318                     120                 125                 130
320  CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC      546
321  Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr
322                 135                 140                 145
324  AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT      594
325  Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu
326         150                 155                 160
328  CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT      642
329  Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
330  165                 170                 175                 180
332  GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA      690
333  Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly
334                     185                 190                 195
336  TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT      738
337  Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile
338                     200                 205                 210
340  TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC      786
341  Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe
342                     215                 220                 225
344  ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT      834
```

**VERIFICATION SUMMARY**                      DATE: 04/10/2002
PATENT APPLICATION:   US/09/714,792      TIME: 18:20:45

Input Set : **N:\jumbos\714792.txt**
Output Set: **N:\CRF3\04102002\I714792.raw**

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:480 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5
L:495 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:525 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:540 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9